* *
Reviewer Comments:
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<213>   Homo sapiens

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Gly Cys Arg Ser Asp Gly Thr Cys Val Cys Lys Pro Gly Phe Gly Gly
            20   25   30

Pro Asn Cys Glu His Gly Ala Phe Ser
        35   40

1

Please remove the above "1," which appears at the end of the submmitted file.

* *

Application No: 10580101   Version No: 1.0

Input Set:

Output Set:

Started: 2007-11-29 13:01:31.530
Finished: 2007-11-29 13:01:33.052
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 522 ms
Total Warnings: 0
Total Errors: 8
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

Error code	Error Description
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E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (10)

<110>   Tryggvason, Karl
        Salo, Sirpa

<120>   Use of antibodies to the gamma 2 chain of laminin 5 to inhibit tumor
        growth and metastasis

<130>   02-1147

<140>   10580101
<141>   2007-11-29

<150>   60/422,009
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<150>   US 09/756,071
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atg cct gcg ctc tgg ctg ggc tgc tgc ctc tgc ttc tcg ctc ctc ctg   165
Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
1   5   10   15

ccc gca gcc cgg gcc acc tcc agg agg gaa gtc tgt gat tgc aat ggg   213
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
            20   25   30

aag tcc agg cag tgt atc ttt gat cgg gaa ctt cac aga caa act ggt   261
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
        35   40   45

aat gga ttc cgc tgc ctc aac tgc aat gac aac act gat ggc att cac   309
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His

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tgc gag aag tgc aag aat ggc ttt tac cgg cac aga gaa agg gac cgc    357
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
65           70              75              80

tgt ttg ccc tgc aat tgt aac tcc aaa ggt tct ctt agt gct cga tgt    405
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
            85              90              95

gac aac tct gga cgg tgc agc tgt aaa cca ggt gtg aca gga gcc aga    453
Asp Asn Ser Gly Arg Cys Ser Cys Lys Pro Gly Val Thr Gly Ala Arg
            100             105             110

tgc gac cga tgt ctg cca ggc ttc cac atg ctc acg gat gcg ggg tgc    501
Cys Asp Arg Cys Leu Pro Gly Phe His Met Leu Thr Asp Ala Gly Cys
        115             120             125

acc caa gac cag aga ctg cta gac tcc aag tgt gac tgt gac cca gct    549
Thr Gln Asp Gln Arg Leu Leu Asp Ser Lys Cys Asp Cys Asp Pro Ala
        130             135             140

ggc atc gca ggg ccc tgt gac gcg ggc cgc tgt gtc tgc aag cca gct    597
Gly Ile Ala Gly Pro Cys Asp Ala Gly Arg Cys Val Cys Lys Pro Ala
145             150             155             160

gtt act gga gaa cgc tgt gat agg tgt cga tca ggt tac tat aat ctg    645
Val Thr Gly Glu Arg Cys Asp Arg Cys Arg Ser Gly Tyr Tyr Asn Leu
                165             170             175

gat ggg ggg aac cct gag ggc tgt acc cag tgt ttc tgc tat ggg cat    693
Asp Gly Gly Asn Pro Glu Gly Cys Thr Gln Cys Phe Cys Tyr Gly His
            180             185             190

tca gcc agc tgc cgc agc tct gca gaa tac agt gtc cat aag atc acc    741
Ser Ala Ser Cys Arg Ser Ser Ala Glu Tyr Ser Val His Lys Ile Thr
        195             200             205

tct acc ttt cat caa gat gtt gat ggc tgg aag gct gtc caa cga aat    789
Ser Thr Phe His Gln Asp Val Asp Gly Trp Lys Ala Val Gln Arg Asn
    210             215             220

ggg tct cct gca aag ctc caa tgg tca cag cgc cat caa gat gtg ttt    837
Gly Ser Pro Ala Lys Leu Gln Trp Ser Gln Arg His Gln Asp Val Phe
225             230             235             240

agc tca gcc caa cga cta gat cct gtc tat ttt gtg gct cct gcc aaa    885
Ser Ser Ala Gln Arg Leu Asp Pro Val Tyr Phe Val Ala Pro Ala Lys
        245             250             255

ttt ctt ggg aat caa cag gtg agc tat ggg caa agc ctg tcc ttt gac    933
Phe Leu Gly Asn Gln Gln Val Ser Tyr Gly Gln Ser Leu Ser Phe Asp
            260             265             270

tac cgt gtg gac aga gga ggc aga cac cca tct gcc cat gat gtg atc    981
Tyr Arg Val Asp Arg Gly Gly Arg His Pro Ser Ala His Asp Val Ile
        275             280             285
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ctg gaa ggt gct ggt cta cgg atc aca gct ccc ttg atg cca ctt ggc     1029
Leu Glu Gly Ala Gly Leu Arg Ile Thr Ala Pro Leu Met Pro Leu Gly
    290             295             300

aag aca ctg cct tgt ggg ctc acc aag act tac aca ttc agg tta aat     1077
Lys Thr Leu Pro Cys Gly Leu Thr Lys Thr Tyr Thr Phe Arg Leu Asn
305             310             315             320

gag cat cca agc aat aat tgg agc ccc cag ctg agt tac ttt gag tat     1125
Glu His Pro Ser Asn Asn Trp Ser Pro Gln Leu Ser Tyr Phe Glu Tyr
            325             330             335

cga agg tta ctg cgg aat ctc aca gcc ctc cgc atc cga gct aca tat     1173
Arg Arg Leu Leu Arg Asn Leu Thr Ala Leu Arg Ile Arg Ala Thr Tyr
            340             345             350

gga gaa tac agt act ggg tac att gac aat gtg acc ctg att tca gcc     1221
Gly Glu Tyr Ser Thr Gly Tyr Ile Asp Asn Val Thr Leu Ile Ser Ala
            355             360             365

cgc cct gtc tct gga gcc cca gca ccc tgg gtt gaa cag tgt ata tgt     1269
Arg Pro Val Ser Gly Ala Pro Ala Pro Trp Val Glu Gln Cys Ile Cys
    370             375             380

cct gtt ggg tac aag ggg caa ttc tgc cag gat tgt gct tct ggc tac     1317
Pro Val Gly Tyr Lys Gly Gln Phe Cys Gln Asp Cys Ala Ser Gly Tyr
385             390             395             400

aag aga gat tca gcg aga ctg ggg cct ttt ggc acc tgt att cct tgt     1365
Lys Arg Asp Ser Ala Arg Leu Gly Pro Phe Gly Thr Cys Ile Pro Cys
            405             410             415

aac tgt caa ggg gga ggg gcc tgt gat cca gac aca gga gat tgt tat     1413
Asn Cys Gln Gly Gly Gly Ala Cys Asp Pro Asp Thr Gly Asp Cys Tyr
            420             425             430

tca ggg gat gag aat cct gac att gag tgt gct gac tgc cca att ggt     1461
Ser Gly Asp Glu Asn Pro Asp Ile Glu Cys Ala Asp Cys Pro Ile Gly
            435             440             445

ttc tac aac gat ccg cac gac ccc cgc agc tgc aag cca tgt ccc tgt     1509
Phe Tyr Asn Asp Pro His Asp Pro Arg Ser Cys Lys Pro Cys Pro Cys
    450             455             460

cat aac ggg ttc agc tgc tca gtg att ccg gag acg gag gag gtg gtg     1557
His Asn Gly Phe Ser Cys Ser Val Ile Pro Glu Thr Glu Glu Val Val
465             470             475             480

tgc aat aac tgc cct ccc ggg gtc acc ggt gcc cgc tgt gag ctc tgt     1605
Cys Asn Asn Cys Pro Pro Gly Val Thr Gly Ala Arg Cys Glu Leu Cys
            485             490             495

gct gat ggc tac ttt ggg gac ccc ttt ggt gaa cat ggc cca gtg agg     1653
Ala Asp Gly Tyr Phe Gly Asp Pro Phe Gly Glu His Gly Pro Val Arg
            500             505             510
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cct tgt cag ccc tgt caa tgc aac agc aat gtg gac ccc agt gcc tct      1701
Pro Cys Gln Pro Cys Gln Cys Asn Ser Asn Val Asp Pro Ser Ala Ser
        515                 520                 525

ggg aat tgt gac cgg ctg aca ggc agg tgt ttg aag tgt atc cac aac      1749
Gly Asn Cys Asp Arg Leu Thr Gly Arg Cys Leu Lys Cys Ile His Asn
    530                 535                 540

aca gcc ggc atc tac tgc gac cag tgc aaa gca ggc tac ttc ggg gac      1797
Thr Ala Gly Ile Tyr Cys Asp Gln Cys Lys Ala Gly Tyr Phe Gly Asp
545                 550                 555                 560

cca ttg gct ccc aac cca gca gac aag tgt cga gct tgc aac tgt aac      1845
Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Arg Ala Cys Asn Cys Asn
                565                 570                 575

ccc atg ggc tca gag cct gta gga tgt cga agt gat ggc acc tgt gtt      1893
Pro Met Gly Ser Glu Pro Val Gly Cys Arg Ser Asp Gly Thr Cys Val
                580                 585                 590

tgc aag cca gga ttt ggt ggc ccc aac tgt gag cat gga gca ttc agc      1941
Cys Lys Pro Gly Phe Gly Gly Pro Asn Cys Glu His Gly Ala Phe Ser
        595                 600                 605

tgt cca gct tgc tat aat caa gtg aag att cag atg gat cag ttt atg      1989
Cys Pro Ala Cys Tyr Asn Gln Val Lys Ile Gln Met Asp Gln Phe Met
    610                 615                 620

cag cag ctt cag aga atg gag gcc ctg att tca aag gct cag ggt ggt      2037
Gln Gln Leu Gln Arg Met Glu Ala Leu Ile Ser Lys Ala Gln Gly Gly
625                 630                 635                 640

gat gga gta gta cct gat aca gag ctg gaa ggc agg atg cag cag gct      2085
Asp Gly Val Val Pro Asp Thr Glu Leu Glu Gly Arg Met Gln Gln Ala
                645                 650                 655

gag cag gcc ctt cag gac att ctg aga gat gcc cag att tca gaa ggt      2133
Glu Gln Ala Leu Gln Asp Ile Leu Arg Asp Ala Gln Ile Ser Glu Gly
                660                 665                 670

gct agc aga tcc ctt ggt ctc cag ttg gcc aag gtg agg agc caa gag      2181
Ala Ser Arg Ser Leu Gly Leu Gln Leu Ala Lys Val Arg Ser Gln Glu
        675                 680                 685

aac agc tac cag agc cgc ctg gat gac ctc aag atg act gtg gaa aga      2229
Asn Ser Tyr Gln Ser Arg Leu Asp Asp Leu Lys Met Thr Val Glu Arg
    690                 695                 700

gtt cgg gct ctg gga agt cag tac cag aac cga gtt cgg gat act cac      2277
Val Arg Ala Leu Gly Ser Gln Tyr Gln Asn Arg Val Arg Asp Thr His
705                 710                 715                 720

agg ctc atc act cag atg cag ctg agc ctg gca gaa agt gaa gct tcc      2325
Arg Leu Ile Thr Gln Met Gln Leu Ser Leu Ala Glu Ser Glu Ala Ser
                725                 730                 735

ttg gga aac act aac att cct gcc tca gac cac tac gtg ggg cca aat      2373
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Leu Gly Asn Thr Asn Ile Pro Ala Ser Asp His Tyr Val Gly Pro Asn
            740             745             750

ggc ttt aaa agt ctg gct cag gag gcc aca aga tta gca gaa agc cac    2421
Gly Phe Lys Ser Leu Ala Gln Glu Ala Thr Arg Leu Ala Glu Ser His
            755             760             765

gtt gag tca gcc agt aac atg gag caa ctg aca agg gaa act gag gac    2469
Val Glu Ser Ala Ser Asn Met Glu Gln Leu Thr Arg Glu Thr Glu Asp
            770             775             780

tat tcc aaa caa gcc ctc tca ctg gtg cgc aag gcc ctg cat gaa gga    2517
Tyr Ser Lys Gln Ala Leu Ser Leu Val Arg Lys Ala Leu His Glu Gly
785             790             795             800

gtc gga agc gga agc ggt agc ccg gac ggt gct gtg gtg caa ggg ctt    2565
Val Gly Ser Gly Ser Gly Ser Pro Asp Gly Ala Val Val Gln Gly Leu
                805             810             815

gtg gaa aaa ttg gag aaa acc aag tcc ctg gcc cag cag ttg aca agg    2613
Val Glu Lys Leu Glu Lys Thr Lys Ser Leu Ala Gln Gln Leu Thr Arg
            820             825             830

gag gcc act caa gcg gaa att gaa gca gat agg tct tat cag cac agt    2661
Glu Ala Thr Gln Ala Glu Ile Glu Ala Asp Arg Ser Tyr Gln His Ser
            835             840             845

ctc cgc ctc ctg gat tca gtg tct ccg ctt cag gga gtc agt gat cag    2709
Leu Arg Leu Leu Asp Ser Val Ser Pro Leu Gln Gly Val Ser Asp Gln
            850             855             860

tcc ttt cag gtg gaa gaa gca aag agg atc aaa caa aaa gcg gat tca    2757
Ser Phe Gln Val Glu Glu Ala Lys Arg Ile Lys Gln Lys Ala Asp Ser
865             870             875             880

ctc tca agc ctg gta acc agg cat atg gat gag ttc aag cgt aca caa    2805
Leu Ser Ser Leu Val Thr Arg His Met Asp Glu Phe Lys Arg Thr Gln
                885             890             895

aag aat ctg gga aac tgg aaa gaa gaa gca cag cag ctc tta cag aat    2853
Lys Asn Leu Gly Asn Trp Lys Glu Glu Ala Gln Gln Leu Leu Gln Asn
                900             905             910

gga aaa agt ggg aga gag aaa tca gat cag ctg ctt tcc cgt gcc aat    2901
Gly Lys Ser Gly Arg Glu Lys Ser Asp Gln Leu Leu Ser Arg Ala Asn
            915             920             925

ctt gct aaa agc aga gca caa gaa gca ctg agt atg ggc aat gcc act    2949
Leu Ala Lys Ser Arg Ala Gln Glu Ala Leu Ser Met Gly Asn Ala Thr
            930             935             940

ttt tat gaa gtt gag agc atc ctt aaa aac ctc aga gag ttt gac ctg    2997
Phe Tyr Glu Val Glu Ser Ile Leu Lys Asn Leu Arg Glu Phe Asp Leu
945             950             955             960

cag gtg gac aac aga aaa gca gaa gct gaa gaa gcc atg aag aga ctc    3045
Gln Val Asp Asn Arg Lys Ala Glu Ala Glu Glu Ala Met Lys Arg Leu
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tcc tac atc agc cag aag gtt tca gat gcc agt gac aag acc cag caa   3093
Ser Tyr Ile Ser Gln Lys Val Ser Asp Ala Ser Asp Lys Thr Gln Gln
        980   985   990

gca gaa aga gcc ctg ggg agc gct gct gct gat gca cag agg gca aag   3141
Ala Glu Arg Ala Leu Gly Ser Ala Ala Ala Asp Ala Gln Arg Ala Lys
        995   1000   1005

aat ggg gcc ggg gag gcc ctg gaa atc tcc agt gag att gaa cag   3186
Asn Gly Ala Gly Glu Ala Leu Glu Ile Ser Ser Glu Ile Glu Gln
   1010   1015   1020

gag att ggg agt ctg aac ttg gaa gcc aat gtg aca gca gat gga   3231
Glu Ile Gly Ser Leu Asn Leu Glu Ala Asn Val Thr Ala Asp Gly
   1025   1030   1035

gcc ttg gcc atg gaa aag gga ctg gcc tct ctg aag agt gag atg   3276
Ala Leu Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met
   1040   1045   1050

agg gaa gtg gaa gga gag ctg gaa agg aag gag ctg gag ttt gac   3321
Arg Glu Val Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp
   1055   1060   1065

acg aat atg gat gca gta cag atg gtg att aca gaa gcc cag aag   3366
Thr Asn Met Asp Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys
   1070   1075   1080

gtt gat acc aga gcc aag aac gct ggg gtt aca atc caa gac aca   3411
Val Asp Thr Arg Ala Lys Asn Ala Gly Val Thr Ile Gln Asp Thr
   1085   1090   1095

ctc aac aca tta gac ggc ctc ctg cat ctg atg gac cag cct ctc   3456
Leu Asn Thr Leu Asp Gly Leu Leu His Leu Met Asp Gln Pro Leu
   1100   1105   1110

agt gta gat gaa gag ggg ctg gtc tta ctg gag cag aag ctt tcc   3501
Ser Val Asp Glu Glu Gly Leu Val Leu Leu Glu Gln Lys Leu Ser
   1115   1120   1125

cga gcc aag acc cag atc aac agc caa ctg cgg ccc atg atg tca   3546
Arg Ala Lys Thr Gln Ile Asn Ser Gln Leu Arg Pro Met Met Ser
   1130   1135   1140

gag ctg gaa gag agg gca cgt cag cag agg ggc cac ctc cat ttg   3591
Glu Leu Glu Glu Arg Ala Arg Gln Gln Arg Gly His Leu His Leu
   1145   1150   1155

ctg gag aca agc ata gat ggg att ctg gct gat gtg aag aac ttg   3636
Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala Asp Val Lys Asn Leu
   1160   1165   1170

gag aac att agg gac aac ctg ccc cca ggc tgc tac aat acc cag   3681
Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys Tyr Asn Thr Gln
   1175   1180   1185

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gct ctt  gag caa cag tga agctgccata aatatttctc aactgaggtt                3729
Ala Leu  Glu Gln Gln
     1190


cttgggatac agatctcagg gctcgggagc catgtcatgt gagtgggtg
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